

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Timothy A.
Rosen, Craig A.
- (ii) TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide III

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Human Genome Sciences, Inc.
- (B) STREET: 9410 Key West Avenue
- (C) CITY: Rockville,
- (D) STATE: MD
- (E) COUNTRY: USA
- (F) ZIP: 20850

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/972,301
- (B) FILING DATE: 18-NOV-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/483,534
- (B) FILING DATE: 07-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Marks, Michelle S.
- (B) REGISTRATION NUMBER: 41,971
- (C) REFERENCE/DOCKET NUMBER: PF206D1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 301-309-8504
- (B) TELEFAX: 301-309-8439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 94..597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TACCCCTGCC	CTGAAAAAAC	TGGCCAGCGC	TGCCTACCCA	GATCCCTCAA	AGCAGAAGCC	60
AATGGCCAAA	GGCCTGCCAA	GAATTCAGAA	CCA	GAG GAG GTC ATC CCA TCC CGG		114
				Glu Glu Val Ile Pro Ser Arg		
			1		5	
CTG GAT ATC CGT GTG GGG AAA ATC ATC ACT GTG GAG AAG CAC CCA GAT						162
Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp						
10	15		20			
GCA GAC AGC CTG TAT GTA GAG AAG ATT GAC GTG GGG GAA GCT GAA CCA						210
Ala Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro						
25	30		35			
CGG ACT GTG GTG AGC GGC CTG	GTA	CAG TTC GTG CCC AAG GAG GAA CTG				258
Arg Thr Val Val Ser Gly Leu	Val	Gln Phe Val Pro Lys Glu Glu Leu				
40	45	50	55			
CAG GAC AGG CTG GTA GTG GTG	CTG	TGC AAC CTG AAA CCC CAG AAG ATG				306
Gln Asp Arg Leu Val Val Val	Leu	Cys Asn Leu Lys Pro Gln Lys Met				
60	65	70				
AGA GGA GTC GAG TCC CAA GGC ATG CTT CTG TGT GCT TCT ATA GAA GGG						354
Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly						
75	80	85				
ATA AAC CGC CAG GTT GAA CCT CTG	GAC CCT CCG GCA GGC TCT GCT CCT					402
Ile Asn Arg Gln Val Glu Pro Leu	Asp Pro Pro Ala Gly Ser Ala Pro					
90	95	100				
GGT GAG CAC GTG TTT GTG AAG GGC	TAT GAA AAG GGC CAA CCA GAT GAG					450
Gly Glu His Val Phe Val Lys Gly	Tyr Glu Lys Gly Gln Pro Asp Glu					
105	110	115				
GAG CTC AAG CCC AAG AAG AAA GTC	TTC GAG AAG TTG CAG GCT GAC TTC					498
Glu Leu Lys Pro Lys Lys Val	Phe Glu Lys Leu Gln Ala Asp Phe					
120	125	130	135			
AAA ATT TCT GAG GAG TGC ATC GCA	CAG TGG AAG CAA ACC AAC TTC ATG					546
Lys Ile Ser Glu Glu Cys Ile Ala	Gln Trp Lys Gln Thr Asn Phe Met					
140	145	150				
ACC AAG CTG GGC TCC ATT TCC TGT AAA	TCG CTG AAA GGG GGG AAC ATT					594
Thr Lys Leu Gly Ser Ile Ser Cys Lys	Ser Leu Lys Gly Gly Asn Ile					
155	160	165				
AGC TAGCCAGCCC AGCATCTTCC CCCCTTCTTC CACCACTGA						636
Ser						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile
 1 5 10 15

Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile
 20 25 30

Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu Val Gln
 35 40 45

Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val Leu Cys
 50 55 60

Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly Met Leu
 65 70 75 80

Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro Leu Asp
 85 90 95

Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys Gly Tyr
 100 105 110

Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys Val Phe
 115 120 125

Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln
 130 135 140

Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser Cys Lys
 145 150 155 160

Ser Leu Lys Gly Gly Asn Ile Ser
 165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCGGATCC GAGGAGGTCA TCCCCATCC

28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCAAGCTT CTAGATAATG TTCCCCCCC

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC GAGGAGGTCA TCCCCATCC

28

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCGGATCC CTAGATAATG TTCCCCCCC

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser Ala
1 5 10 15

Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly Cys
20 25 30

Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu
35 40 45

Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly Leu
50 55 60

Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile Leu
65 70 75 80

Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Lys Ser Gln Ala
85 90 95

Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala Pro
100 105 110

Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe Pro
115 120 125

Gly Glu Pro Asp Lys Glu Lys Asn Pro Lys Lys Lys Ile Trp Glu Gln
130 135 140

Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr Lys
145 150 155 160

Glu Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln Thr
165 170 175

Met Ser Asn Ser Gly Ile Lys
180

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X2
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